MBE Author-Subject Index
Volume 11

A+T region, 523
Acanthamoeba, 684
ADACHI, J., 593
Adaptive radiation, 691, 854
Additive trees, 961
ADEY, N. B., 778
Adh, 443
African river blindness, 384
African trypanosomes, 220
AKBARZADE, J., 864
Alcohol dehydrogenase, 287
Allelic genealogy, 803
Allozymes, 737
Alpha A-crystallin, 711
Alpha-2 macroglobulin, 417
Alternative promoter, 305
Alu, 749
ALVAREZ, F., 790
Amino acid sequence, 99
Amniotes, 329, 605
Amphipathic helix, 964
Ancestral polymorphism, 341
Animals, 762
Anopheles nuneztovari, 406
AOYAMA, K., 829
Approximate bootstrap probability, 142
AQUADRO, C. F., 169, 183, 539, 806
ARNOLD, G., 630
ARNOLD, J., 208
ARNTZEN, J. W., 737
Arthropods, 493
Artiodactyla, 357
Artiodactyls, 239
Arylphorin, 493
Ascospore, 376
ASHBURNER, M., 287
ATCHLEY, W. R., 949
Avian phylogeny, 711

BAKER, A., 22
BAKER, A. J., 9
BAKER, S. C., 426
Baleen whales, 939
BALTZ, T., 220
BARGELLONI, L., 854
Bark weevil, 183
BATTAGLIA, B., 854
BEGUN, D., 806
BEINTEMA, J., 493
BESSEN, D. E., 208
bgl operon, 159
Bias of G+C content, 65
Bilateria, 648
Biochemical convergence, 921
Biochemical diversity, 106
Biological rhythms, 839
Birth-and-death process, 469
Bombyx mori, 72
BORRAS, T., 305
Borrelia burgdorferi, 51
BOYCE, T. M., 183
BOYER, S. N., 806
BRINGAUD, F., 220
BROWN, J., 128
Bufo, 737
BUITKAMP, J., 239
BURKE, T., 737
BYERS, T., 684

C3, 417
C4, 417
C5, 417
Calcium-binding lysozyme, 921
Canids, 553
CAO, Y., 593
CAPORALE, D. A., 51
CASEY, R., 325
CASPERS, G.-J., 711
Catadromous fish, 250
Caviomorpha, 593
Ceratocystiopsis, 376
Ceratocystis, 376
Cetacea, 357
CHAKRABORTY, R., 120
CHANG, H. J., 548
CHANG, H. Y., 250
Chaperones, 106
CHEN, C. T., 250
Chi sites, 813
Chicken (*Gallus gallus*), 886
CHINNAPPA, C. C., 365
Chloroplast DNA, 769
Chloroplast genes, 231
Chloroplast origins, 605
Chordates, 648
Chorion gene families, 72
Choristoneura fumiferana, 656
CLARK, J. B., 40
Cluster algorithm, 384
Coalescence, 803
Coancestry coefficient, 949
COCKBURN, A., 406
Codon bias, 231
Codon usage, 790
Codon evolution, 715
Coefficient of gene diversity, 120
COLLET, C., 643
Color vision, 32
Comparison, 571
Compatiblility, 459
Complement components, 417
Computer simulation, 99, 459

Concerted evolution, 9, 393
CONN, J., 406
Control region, 691
Control region sequence, 22
Convergent evolution, 899
Covariance matrix, 630
Covariances, 613
CpDNA, 715
Cps, 829
CR1, 886
CRAWFORD, A., 239
CREISSEN, G., 325
Cryptic species, 406
CUMMINGS, M. P., 1
CURTISS, S. W., 443
Cut, 806
Cystic fibrosis transmembrane conductance regulator, 899
Cytochrome b, 691, 939
Cytochrome c cDNA, 365

Drosophila, 287, 443, 666, 839
Drosophila athabasca, 169
Drosophila evolution, 40
Drosophila melanogaster, 513, 523, 806
Drosophila simulans, 806
D-loop, 9
DE JONG, W. W., 711
DESALLE, R., 393
Determinants, 605
Deuterostome, 648
Direct sequencing, 51
Directed mutation, 159
Distance methods, 961
Divergence, 666
Divergent evolution, 469
DNA fingerprint, 120
DNA polymorphism, 666, 806
DNA sequences, 278
DOLAN, B., 146
Domain, 99
DOMONEY, C., 325

Escherichia coli, 159, 829
EASTEAL, S., 643
EDE, A. J., 239
EDGELL, M. H., 778
EDWARDS, A. R., 911
Effective population number, 803
18S-like rRNA sequences, 684
18S rRNA, 648
18S rRNA genes, 195
ELLSWORTH, D. L., 875
Elongation factor 1-alpha, 65
Endosymbiotic theory, 899
EPPLEN, J. T., 239
Estimation method, 154
Eudromia elegans, 711

Eukaryotes, 65
Evolution, 443, 493, 778, 790, 875, 886
Evolutionary distance, 99, 278
Evolutionary model(s), 605, 715
Eolutionary opportunism, 964
Evolutionary rate, 504
Evolutionary trees, 605
Exon, 341
Extinction and recolonization, 803
Eye lens, 711
EYRE-WALKER, A., 88

FARQUHAR, A. L., 523
FARR, C. L., 523
FELSENSTEIN, J., 459
Fish, 106
FITCH, W. M., 571, 949
FITCH-MARGOLIASH, 459
5S ribosomal DNA, 704
Foraminifera, 929
FORD, M. J., 169
Foregut fermentation, 921
FORSTER, C., 325
FRIDAY, A., 316
FRIEDLANDER, T. P., 72
FRITZ, G. N., 406
Fucose pathway, 829
FUERST, P. A., 684
FUKAMI-KOBAYASHI, K., 99
Fungi, 762

G+C content, 88, 829
Gamma distribution, 316, 436
GASCUEL, O., 961
GAST, R. J., 684
GAUT, B., 620
GAUT, B. S., 715
GC content, 875
GEFFEN, E., 553
Gene cluster, 208
Gene conversion, 72, 548
Gene flow, 553
Gene genealogy, 803
Genetic distance(s), 120, 949
Genetic drift, 949
Genetic hitchhiking, 539
Genetic variability, 737
Genetic variation, 553
Giardia lamblia, 65
GIELLY, L., 769
Glucose transporter genes, 220
GOLDMAN, N., 316, 725
GONZALEZ, P., 305
GRAHAM, D. K., 778
GRANT, W. S., 376
GRAUR, D., 357
Greya, 128
Group I introns, 195
Guinea pig, 305, 593

HAASE, A. M., 829
Hadamard conjugations, 630
HALL, B. G., 159
HAMMER, M. F., 749
HANNEL, J., 864
HARRISON, R. G., 128
Hartmannella, 684
HASEGAWA, M., 142, 593
HAUSER, M. T., 513
HAYASE, N., 762
HAZES, B., 493
Heat shock proteins, 106
HEIDEMAN, A., 341
Hemocyanin, 493
Hemoglobin, 854
HENDY, M., 630
HENDY, M. D., 605
HERNANDEZ-CALZADILLA, C., 305
HEWETT-EMMETT, D., 875
Hexamerins, 493
HICKEY, D. A., 656
HIGGINS, D. G., 357
HIGHTOWER, L. E., 106
Hitchhiking, 169, 666
Hoatzin, 921
HOLLINGSHEAD, S. K., 208
HOLMES, E. C., 287
Homology, 964
Honeybees, 605
Horizontal gene transfer, 40
Horizontal transfer, 911
HUGALL, A., 672
HUGHES, A., 417, 899
HUI, C.-F., 250
Human, 749
Human population, 803
HUTCHISON, C. A. III, 778
Hybridization, 183, 553

Icefish, 854
Ice nucleation, 911
IKEDA, H., 864
Immune system evolution, 417
Immunoglobulin, 469
Imprinting, 875
Initiation codon, 329
Insects, 493
Insertions-deletions, 504, 769
Insulin-like growth factors, 875
Internal transcribed spacer(s), 393, 513
Internal transcribed spacer region, 620
Internal transcribed spacer 2, 406
Intron(s), 325, 341, 426
Intron evolution, 239, 548
Intron mobility, 195
Introns, 325
IS150, 159
Island model, 803
Isochore, 875
IWABE, N., 762

JAMIESON, B. G. M., 672
JEFFS, P. S., 287
JIN, L., 120
JIN, M.-L., 864
Jukes and Cantor's method, 278

KAGUNI, L. S., 523
KATHOLI, C. R., 384
KELLOGG, E. A., 1
KIDWELL, M., 40
Kimura's method, 278
Kineoplastid, 790
KING, L. M., 1
KISHINO, H., 142
KOCHER, T., 51
KORNEGAY, J. R., 921
KRYUKOV, A. P., 864
KUHNER, M. K., 459
KUMA, K.-i., 762
KWOK, W., 666
KYRIACOU, C. P., 839

L1, 778
LAMBERT, D. M., 854
Lamprologini, 691
LAN, R., 813
LANG, B. F., 329
LANG-UNNASCH, N., 384
Lateral gene, 813
Lateral gene transfer, 813
Lateral transfer, 829
LECLERC, R. F., 72
LEWIS, D. L., 523
LI, L., 548
LI, W.-H., 548, 875
Likelihood ratio, 620, 715
LINEs, 778
LOCKHART, P. J., 605
Large subunit, 929
LUNDRIGAN, B. L., 483
Lyme disease, 51

M protein, 208
MCCLURE, M. A., 571
MADDISON, W., 40
Mammalian evolution, 593
Mammalian transposable element, 778
Mammals, 643
Mannose pathway, 829
Marchantia polymorpha, 231
Marine red algae, 195
Mariner transposable elements, 620
Mating song, 169
MATTA, N., 325
MATULONIS, P., 666

Maximum likelihood, 99, 142, 154, 316, 459, 762
Maximum-likelihood method, 261
Maximum-likelihood tree of proteins, 593
Maximum parsimony, 261, 762
Melanotaeniidae, 672
MENOTTI-RAYMOND, M., 443
Metabolic rate, 854
MEYER, A., *691*, *854*, *939*
MHC complex, 239
Mice, 704
Microsatellites, 553, 737
MILINKOVITCH, M. C., 939
MINDELL, D., 329
Minimum-evolution principle, 961
Minisatellites, 737
Mismatch repair, 88
Mitochondria, 656, 964
Mitochondrial ribosomal DNA, 939
Mitochondrial DNA (mtDNA), *22*, 128, 154, 183, 250, 329, 426, 436, 523, 672
MIYASHITA, M., 864
MIYATA, T., 762
Mobile DNA, *40*
Models, 316, 725
Molecular and morphological phylogenies, 128
Molecular adaptation, *921*
Molecular clock, 504, 643
Molecular evolution, *1*, *32*, *208*, *220*, *305*, 704, 711, 911
Molecular evolutionary tree, 142
Molecular phylogenetic tree, 278
Molecular phylogeny, *357*, *762*, *929*
Molecular systematics, 483
MORAIS, R., 329
MORITZ, C., 341, 672
MORIWAKI, K., 704, 864
Morphology, 648
Mouse, 146, 305
Multigene family, 220, 469
Multiple alignment , 571
Mus, 483
Mus domesticus, 539
Mus mus domesticus, 864
Mus musculus, 146, 854
Mus spicilegus, 146
Mus spretus, 146
MUSE, S. V., 715
Mutational pressure, 790
Mutation rate, 88, 504, 643, 899

NACHMAN, M. W., 539
NAGAMONE, C. M., 864
NAKAMURA, F., *65*
NAKAMURA, Y., 65
NEI, M., *261*, *469*, *613*
Neighbor-joining, 459, 762
Neighbor-joining method, *261*
Neighborliness, 961
NEILSEN, J., 839
Neutral evolution, 513
Neutral mutation, 250
Neutral theory, 643
NIKOH, N., 762
NISHIOKA, Y., 146
Noncoding regions, 769
Non-LTR retrotransposition, 886
Nonsynonymous substitutions, 613, 725
Nucleotide substitution(s), *154*, *316*, *620*, 725
Nucleotide composition, *605*
Nyssorhynchus, *406*

Ocular lens, 305
OLIVEIRA, M. C., 195
Onchocerca volvulus, 384
Ophiostoma, 376
ORSER, C. S., 911
OSTRANDER, E., 553
OTA, T., 469, 613
Outer surface protein genes, 51

P elements, 40
P-glycoprotein, *899*
Palaeognatheae, 711
PALUMBI, S. R., 426
PAO, G. M., 964
Paralogy, 365
Parsimony, 459, 749
PATARNELOO, T., 854
Pattern of nucleotide substitution, 128
PAWLOWSKI, J., 929
Pecora, 357
PELLMYR, O., 128
PENNY, D., 605, 630
Period, 169
Period gene, 839
PETERSON, S. N., 778
Phenetics, 384
Phylogenetic analysis, 40, 672, 886, 911
Phylogenetic estimation, 725
Phylogenetic inference, 961
Phylogenetic inference, 630
Phylogenetics, 939
Phylogeny, 32, 183, 261, 287, 341, 376, 459, 513, 648, 656, 949
Pissodes, *183*
Pisum savitum, 325
Plant cytochrome c evolution, *365*
Plant-insect interactions, 128
Plants, *762*
Polymerase chain reaction, 51, 341, 393, *426*, *691*, *704*
Polymorphism, 656, 749
Population aggregation analysis, *393*
Population genetic structure, 22
Population genetics, *120*

Population structure, 426, 803
Positive selection, 51
POWELL, J. R., 939
PRADO, V., 146
Primates, 504
Promoter acquisition, 778
Prophyra, 195
Protein-coding sequences, 725
Protein family motifs, 571
Protein phylogeny, 65
Protozoa lacking mitochondria, 65
Prune, 666
Pseudogene, 341, 443

RAFF, R. A., 648
RAGAN, M. A., 195
Random genetic drift, 829
RAO, P. V., 305
Rate of substitution, 231
Rate variation, 436
Rates of divergence, 9
Ratios of random variables, 436
*rbc*L, 769
READDY, T, 208
Recombination, 220
Reduction of heterozygosity, 949
REEVES, P., 829
REEVES, P. R., 813
REIGER, J. C., 72
REITMAN, M., 886
Relative rate test, 715
Repetitive DNA, 839, 886
Repetitive sequence, 146
Repleta, 443
Replication origin, 329
Ribosomal DNA, 406, 513
Ribosomal RNA, 929
Ribosomal RNA sequence analysis, 376
RITCHIE, P. A., 854
RNA polymerase, 1
ROBELLO, C., 790
Rodents, 593
RODRIGUEZ, I. R., 305
ROY, M. S., 553
Ruminantia, 357

Salmonella enterica gnd gene, 813
SAIER, M. H. Jr., 964
SAITOU, N., 504
SAKURAI, S., 704
SANG, T. K., 250
SCHICHMAN, S. A., 778
SCHILLING, J. W., 921
SCHLÖTTERER, C., 513
SCHULTZ, R. J., 106
SCHULZ, J. R., 648
SCHWAIGER, F. W., 239
SCRIBNER, K. T., 737
SEAWRIGHT, J., 406
Secondary structure, 513
Selection, 666
Selection and evolution, 813
Selection-induced mutations, 159
Sequence acquisition, 778
Sequence evolution, 672
Sequence spectra, 630
SEUTIN, G., 329
SHIROISHI, T., 864
Shorebirds, 22
SHYUE, S. K., 548
Silent sites, 88
SIMMONS, G. M., 666
16S ribosomal RNA, 854, 911
SLADE, R. W., 341
Slightly deleterious mutations, 643
Small subunit, 929
Small subunit rDNA, 195
Small subunit rRNA phylogeny, 684
SMITH, D., 553
Sorex, 9
Spacer sequences, 704
Spatial rate variation, 316
Spatial variation, 737
Speciation, 656
Species flock, 691
SPERLING, F. A. H., 656
Sperm whales, 939
Sry, 483, 864
STAM, W. T., 493
STARMER, W. T., 443
STEEL, M. A., 605
Stellaria longipes, 365
STEWART, D., 9
Stomach lysozyme, 921
Storage proteins, 493
Streptococcus pyogenes, 208
Stress-70 proteins, 325
STURMBAUER, C., 691
Substitution rate, 88, 643
Suiformes, 357
SULLIVAN, D. T., 443
Synonymous codon use, 88
Synonymous substitutions, 613, 725
Synonymous and nonsynonymous substitutions, 813
Systematics, 1

TABERLET, P., 769
TAJIMA, F., 278
TAKAHATA, N., 803
TAKAO, N., 864
TAKEZAKI, N., 261, 278
TAMURA, K., 154
Tandem repeats, 9, 523
Tandem repeat family, 384
Tap protein, 899
Targeting, 964
TATENO, Y., 261

TAUTZ, D., 513
Testis-determining gene, 864
THAMPAPILLAI, G., 813
THOMAS, H. D., 864
THOMPSON, J. N., 128
TILANUS, M., 22
Time of divergence, 357
Tinamiformes, 711
Tortricidae, 656
Tragulina, 357
Transfer RNA, 329
Transcript, 443
Transition bias, 436
Transition/transversion bias, 278
Trypanosoma, 790
TSUCHIYA, K., 864
TUCKER, P. L., 483
TURBEVILLE, J. M., 648
12S rRNA, 854
Tylopoda, 357
TYSON, H., 146

UEDA, S., 504
UNNASCH, T. R., 384

VAN DEN BUSSCHE, R. A., 911
VANDERGON, T. L., 886
Variances, 613
Varying rate of substitution, 261
VASI, T. K., 571
VENKATESH, T., 666
VERHEYEN, E., 691
Vertebrates, 329, 875
VH genes, 469
VIGNALI, M., 790
Virulence gene family, 208
Visual pigment genes, 548
VNTR loci, 737
VOGLER, A. P., 393
VON HAESELER, A., 513

WADDELL, P., 630
WAKELEY, J., 436
WANG, F.-S., 864
WATTEL, J., 711
WAYNE, R. K., 553
WEEKERS, P., 684
Weighted parsimony, 128
WENINK, P., 22
WEYERS, E., 239
Whales, 426
WHITE, C. N., 106
WICHMAN, H. A., 911
WIEGMANN, B. M., 72
WIER, B. S., 620
WILSON, A. C., 921
WINGFIELD, B. D., 376
WINGFIELD, M. J., 376
WOLFAARDT, J. F., 376
WOOTEN, M. C., 384
WU, X.-L., 864

X-linked, 548
XU, S., 949
XY sex reversal, 864

Y chromosome, 146, 483, 539, 749, 864
YANG, Z., 316, 725
YANO, T., 593
YOKOYAMA, S., 32
YOON, C. K., 169
YUM, J., 443

ZAHED, L., 146
ZHANG, X. H., 365
ZHU, D., 672
ZIGLER, J. S. Jr., 305
ZIMMERMAN, P. A., 384